

SEQUENCE LISTING

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 Maxygen ApS
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<120> NEW INTERFERON BETA-LIKE MOLECULES

<130> 0228us410

<150> US 60/272,116

<151> 2001-02-27

<150> US 60/343,436

<151> 2001-12-21

<150> US 60/302,140

<151> 2001-06-29

<150> US 60/316,170

<151> 2001-08-30

<150> not yet assigned

<151> 2002-02-19

<150> DK PA 2001 00333

<151> 2001-03-01

<150> US 09/648,569

<151> 2000-08-25

<160> 57

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<212> DNA

<213> Homo sapiens

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 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu

1

5

10

ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga	159
Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly	
15 20 25	
ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa	207
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln	
30 35 40	
ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac	255
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp	
45 50 55 60	
atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc	303
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala	
65 70 75	
gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga	351
Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg	
80 85 90	
caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc	399
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu	
95 100 105	
ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa	447
Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu	
110 115 120	
gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt	495
Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser	
125 130 135 140	
ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc	543
Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala	
145 150 155	
aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta	591
Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu	
160 165 170	
agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac	636
Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn	
175 180 185	
tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca	696
gcagatgctg ttttaagtac tgatggctaa tgtactgcat atgaaaggac actagaagat	756
tttgaaattt ttattaaatt atgagttatt tttattttatt taaattttat tttggaaaat	816
aaattatttt tgggtcaaaa gtca	840

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<212> PRT

<213> Homo sapiens

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 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 Thr Gly Tyr Leu Arg Asn
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 <211> 70
 <212> DNA
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<220>
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 ctgctcctgt 70

<210> 4
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aagtagaagt 70

<210> 10

<211> 70
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tcaggtgcag 70

<210> 11
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ggccagcagg 70

<210> 12
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gcggcgtcct 70

<210> 13
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<220>
<223> primer

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cctcggggat gtogaagttc atcctgtcct tcaggcagta ctccaggcgc ccgttcagct 60
gccacaggag 70

<210> 14
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<220>
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ggcgatctgg

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<210> 15

<211> 70

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caccagcatc 70

<210> 16

<211> 70

<212> DNA

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 aatccgccag ctgcagc 77

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 <400> 22
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 <210> 23
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 aagtagaagt 70

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<400> 24
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 <400> 25
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cgcggtatcct tatcagttgc gcag

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<210> 30

<211> 33

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tttaaactgg atccagccac catgaccaac aag

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<211> 39

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cagctgcaga acttcaccaa ggaggacgcc

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cgcggtacca gccaccatga ccaacaagt cctg

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<211> 89

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aagcagctgt ggaacttcac caaggaggac 30

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gagaaggagt tcaacaccac cggcaagctg

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<400> 47
cagcttgccg gtggtgttca cctccttctc

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<400> 49
His His His His His His
1 5

<210> 50
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Met Lys His His His His His His
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1 5 10

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Met Lys His Gln His Gln His Gln His Gln His Gln
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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
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Asp Tyr Lys Asp Asp Asp Lys

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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

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<210> 56

<211> 166

<212> PRT

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<223> Synthetic construct

<400> 56

Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln

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15

Ser Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu

20

25

30

Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln

35

40

45

Asn Phe Thr Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln

50

55

60

Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn

65

70

75

80

Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn

85

90

95

His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Phe Asn Thr

100

105

110

Thr Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg

115

120

125

Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr

130

135

140

Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu

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150

155

160

Thr Gly Tyr Leu Arg Asn

165

<210> 57

<211> 166

<212> PRT
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<220>
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<400> 57

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			20					25					30		
Arg	Asp	Arg	Met	Asn	Phe	Asp	Ile	Pro	Glu	Glu	Ile	Arg	Gln	Leu	Gln
			35				40					45			
Asn	Phe	Thr	Lys	Glu	Asp	Ala	Ala	Leu	Thr	Ile	Tyr	Glu	Met	Leu	Gln
			50				55				60				
Asn	Ile	Phe	Ala	Ile	Phe	Arg	Gln	Asp	Ser	Ser	Ser	Thr	Gly	Trp	Asn
65					70				75					80	
Glu	Thr	Ile	Val	Glu	Asn	Leu	Leu	Ala	Asn	Val	Tyr	His	Gln	Ile	Asn
			85						90					95	
His	Leu	Lys	Thr	Val	Leu	Glu	Glu	Lys	Leu	Glu	Lys	Glu	Phe	Asn	Thr
			100					105					110		
Thr	Gly	Lys	Leu	Met	Ser	Ser	Leu	His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg
			115				120					125			
Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr
			130			135					140				
Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu
145					150				155					160	
Thr	Gly	Tyr	Leu	Arg	Asn										
					165										